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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/972,546

DATE: 02/08/2002
TIME: 12:07:16

Input Set : A:\All16us.app
Output Set: N:\CRF3\02082002\I972546.raw

3 <110> APPLICANT: STRITTMATTER, STEPHEN M.
4 CATE, RICHARD L.
5 SAH, DINAH W.Y.
7 <120> TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS
9 <130> FILE REFERENCE: A116US
11 <140> CURRENT APPLICATION NUMBER: 09/972,546
12 <141> CURRENT FILING DATE: 2001-10-06
14 <150> PRIOR APPLICATION NUMBER: 60/238,361
15 <151> PRIOR FILING DATE: 2000-10-06
17 <160> NUMBER OF SEQ ID NOS: 19
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1260
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <400> SEQUENCE: 1

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28 ctcctggccc tgcccctggc ggccccagc tgcccatgc tctgcacctg ctactcatec 120
29 cgcgccaccg tgagctgcca ggccaacaac ttctcctctg tgccgctgtc cctgccacc 180
30 agcaactcagc gactcttctt gcagaacaac ctcatccgca cgctgcggcc aggcaccttt 240
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33 tcgctggagc ccgacacctt ccaggcgctg gagcggtgc agtcgctgca ttgtaccgc 420
34 tgccagctca gcagcctgcc cggcaacatc ttccgaggcc tggtcagcct gcagtacctc 480
35 tacctccagg agaacagcct gctccacctt caggatgact tgttcgaggc cctggccaac 540
36 ctgagccacc tcttctcca cgggaaccgc ctgcggctgc tcacagagca cgtgtttcgc 600
37 ggctggggca gctggaccg gctgctgctg cacgggaacc ggtgcaggg cgtgcaccgc 660
38 gcggccttcc gcggcctcag ccgcctcacc atcctctacc tgttcaacaa cagcctggcc 720
39 tcgctgcccg gcgaggcgct cgcgcacctg ccctcgctcg agttcctgcg gctcaacgct 780
40 aacccctggg cgtgcgactg ccgcgcgcgg ccgctctggg cctgggtcca gcgcgcgcgc 840
41 gtgtccagct ccgacgtgac ctgcgccacc ccccgaggc gccagggcc agacctgcgc 900
42 gcgctccgcg aggcgcactt ccaggcggtg ccgcccgcgg caccacgcg gccgggcagc 960
43 cgcgcgcgcg gcaacagctc ctccaaccac ctgtacggg tggccgaggc cggggcgccc 1020
44 ccagccgac cctccacctt ctaccgagat ctgcctgcc aagactcgcg gggcgccag 1080
45 ggcggggacg cgcctactga ggacgactac tgggggggct acgggggtga ggaccagcga 1140
46 ggggagcaga tgtgccccgg cgctgcctgc caggcgccc cggactccc aggcctgcg 1200
47 ctctcgccg ggctccccag ccctctgctt tgccctctgc tctggtgcc ccaccacctc 1260
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51 <211> LENGTH: 420
52 <212> TYPE: PRT
53 <213> ORGANISM: Homo sapiens
55 <400> SEQUENCE: 2
56 Met Leu Pro Gly Leu Arg Arg Leu Leu Gln Ala Pro Ala Ser Ala Cys

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57      1              5              10              15
59 Leu Leu Leu Met Leu Leu Ala Leu Pro Leu Ala Ala Pro Ser Cys Pro
60              20              25              30
62 Met Leu Cys Thr Cys Tyr Ser Ser Pro Pro Thr Val Ser Cys Gln Ala
63              35              40              45
65 Asn Asn Phe Ser Ser Val Pro Leu Ser Leu Pro Pro Ser Thr Gln Arg
66      50              55              60
68 Leu Phe Leu Gln Asn Asn Leu Ile Arg Thr Leu Arg Pro Gly Thr Phe
69      65              70              75              80
71 Gly Ser Asn Leu Leu Thr Leu Trp Leu Phe Ser Asn Asn Leu Ser Thr
72              85              90              95
74 Ile Tyr Pro Gly Thr Phe Arg His Leu Gln Ala Leu Glu Glu Leu Asp
75              100              105              110
77 Leu Gly Asp Asn Arg His Leu Arg Ser Leu Glu Pro Asp Thr Phe Gln
78      115              120              125
80 Gly Leu Glu Arg Leu Gln Ser Leu His Leu Tyr Arg Cys Gln Leu Ser
81      130              135              140
83 Ser Leu Pro Gly Asn Ile Phe Arg Gly Leu Val Ser Leu Gln Tyr Leu
84      145              150              155              160
86 Tyr Leu Gln Glu Asn Ser Leu Leu His Leu Gln Asp Asp Leu Phe Ala
87              165              170              175
89 Asp Leu Ala Asn Leu Ser His Leu Phe Leu His Gly Asn Arg Leu Arg
90              180              185              190
92 Leu Leu Thr Glu His Val Phe Arg Gly Leu Gly Ser Leu Asp Arg Leu
93      195              200              205
95 Leu Leu His Gly Asn Arg Leu Gln Gly Val His Arg Ala Ala Phe Arg
96      210              215              220
98 Gly Leu Ser Arg Leu Thr Ile Leu Tyr Leu Phe Asn Asn Ser Leu Ala
99      225              230              235              240
101 Ser Leu Pro Gly Glu Ala Leu Ala Asp Leu Pro Ser Leu Glu Phe Leu
102              245              250              255
104 Arg Leu Asn Ala Asn Pro Trp Ala Cys Asp Cys Arg Ala Arg Pro Leu
105              260              265              270
107 Trp Ala Trp Phe Gln Arg Ala Arg Val Ser Ser Ser Asp Val Thr Cys
108      275              280              285
110 Ala Thr Pro Pro Glu Arg Gln Gly Arg Asp Leu Arg Ala Leu Arg Glu
111      290              295              300
113 Ala Asp Phe Gln Ala Cys Pro Pro Ala Ala Pro Thr Arg Pro Gly Ser
114      305              310              315              320
116 Arg Ala Arg Gly Asn Ser Ser Ser Asn His Leu Tyr Gly Val Ala Glu
117              325              330              335
119 Ala Gly Ala Pro Pro Ala Asp Pro Ser Thr Leu Tyr Arg Asp Leu Pro
120              340              345              350
122 Ala Glu Asp Ser Arg Gly Arg Gln Gly Gly Asp Ala Pro Thr Glu Asp
123              355              360              365
125 Asp Tyr Trp Gly Gly Tyr Gly Gly Glu Asp Gln Arg Gly Glu Gln Met
126      370              375              380
128 Cys Pro Gly Ala Ala Cys Gln Ala Pro Pro Asp Ser Arg Gly Pro Ala
129      385              390              395              400

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131 Leu Ser Ala Gly Leu Pro Ser Pro Leu Leu Cys Leu Leu Leu Leu Val
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134 Pro His His Leu
135                420
138 <210> SEQ ID NO: 3
139 <211> LENGTH: 1383
140 <212> TYPE: DNA
141 <213> ORGANISM: Mus sp.
143 <400> SEQUENCE: 3
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145 ggggtgctgtg tggaattgct gctgttgctg ctcgctggag agctacctct ggggtgggtgg 120
146 tgcctcgag actgtgtgtg ctacctgag cccatgactg tcagctgccg ggcacacaac 180
147 tttgtgcca tcccggagg catcccagag gacagtgagc gcatcttctt gcagaacaat 240
148 cgcacacct tccctccagca gggccacttc agccccgcc tggtcaccct ctggatctac 300
149 tccaacaaca tcactttcat tgctcccaac accttcgagg gctttgtgca tctggaggag 360
150 ctagaacctt gagacaaccg acagctgcga acgctggcac ccgagacctt ccaaggcctg 420
151 gtgaagcttc acgcccctta cctctataag tgtggactga gcgcccctgcc cgcaggcatc 480
152 tttggtggcc tgcacagcct gcagtatctc tacttgagg acaaccatat cgagtacctc 540
153 caagatgaca tctttgtgga cctgggtcaat ctcagtcact tgtttctcca tggtaacaag 600
154 ctatggagcc tgggccaagg catcttcccg ggctgggtga acctggaccg gttgctgctg 660
155 catgagaacc agctacagtg ggttcaccac aaggctttcc atgacctoca caggctaacc 720
156 accctctttc tcttcaacaa cagcctcact gagctgcagg gtgactgtct ggccccctg 780
157 gtggccttgg agttccttcg cctcaatggg aatgcttggg actgtggctg ccgggcacgt 840
158 tccctgtggg aatggctgcg aaggttccgt ggctctagct ctgctgtccc ctgcgcgacc 900
159 cccgagctgc ggcaaggcca ggaatgaaag ctgctgaggg tggaggactt ccggaactgc 960
160 acaggaccag tgtctcctca ccagatcaag tctcacacgc ttaccacctc tgacagggct 1020
161 gcccgaagg agcaccatcc gtcccatggg gctccaggg acaaaggcca cccacatggc 1080
162 catccgctg gctccaggtc aggttacaag aaggcaggca agaactgcac cagccacagg 1140
163 aaccggaacc agatctctaa ggtgagctct gggaaagagc ttaccgaact gcaggactat 1200
164 gccccgact atcagcacia gttcagcttt gacatcatgc ccaccgcag acccaagagg 1260
165 aagggaagt gtgctcgag gacccccatc cgtgccccca gtgggggtgca gcaggcatcc 1320
166 tcaggcacgg cccttggggc cccactcctg gcctggatac tggggctggc agtcactctc 1380
167 cgc
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171 <211> LENGTH: 461
172 <212> TYPE: PRT
173 <213> ORGANISM: Mus sp.
175 <400> SEQUENCE: 4
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177 1 5 10 15
179 Ala Gln Val Ser Gly Cys Cys Val Glu Leu Leu Leu Leu Leu Ala
180 20 25 30
182 Gly Glu Leu Pro Leu Gly Gly Gly Cys Pro Arg Asp Cys Val Cys Tyr
183 35 40 45
185 Pro Ala Pro Met Thr Val Ser Cys Gln Ala His Asn Phe Ala Ala Ile
186 50 55 60
188 Pro Glu Gly Ile Pro Glu Asp Ser Glu Arg Ile Phe Leu Gln Asn Asn
189 65 70 75 80
191 Arg Ile Thr Phe Leu Gln Gln Gly His Phe Ser Pro Ala Met Val Thr

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192          85          90          95
194 Leu Trp Ile Tyr Ser Asn Asn Ile Thr Phe Ile Ala Pro Asn Thr Phe
195          100          105          110
197 Glu Gly Phe Val His Leu Glu Glu Leu Asp Leu Gly Asp Asn Arg Gln
198          115          120          125
200 Leu Arg Thr Leu Ala Pro Glu Thr Phe Gln Gly Leu Val Lys Leu His
201          130          135          140
203 Ala Leu Tyr Leu Tyr Lys Cys Gly Leu Ser Ala Leu Pro Ala Gly Ile
204 145          150          155          160
206 Phe Gly Gly Leu His Ser Leu Gln Tyr Leu Tyr Leu Gln Asp Asn His
207          165          170          175
209 Ile Glu Tyr Leu Gln Asp Asp Ile Phe Val Asp Leu Val Asn Leu Ser
210          180          185          190
212 His Leu Phe Leu His Gly Asn Lys Leu Trp Ser Leu Gly Gln Gly Ile
213          195          200          205
215 Phe Arg Gly Leu Val Asn Leu Asp Arg Leu Leu Leu His Glu Asn Gln
216          210          215          220
218 Leu Gln Trp Val His His Lys Ala Phe His Asp Leu His Arg Leu Thr
219 225          230          235          240
221 Thr Leu Phe Leu Phe Asn Asn Ser Leu Thr Glu Leu Gln Gly Asp Cys
222          245          250          255
224 Leu Ala Pro Leu Val Ala Leu Glu Phe Leu Arg Leu Asn Gly Asn Ala
225          260          265          270
227 Trp Asp Cys Gly Cys Arg Ala Arg Ser Leu Trp Glu Trp Leu Arg Arg
228          275          280          285
230 Phe Arg Gly Ser Ser Ser Ala Val Pro Cys Ala Thr Pro Glu Leu Arg
231          290          295          300
233 Gln Gly Gln Asp Leu Lys Leu Leu Arg Val Glu Asp Phe Arg Asn Cys
234 305          310          315          320
236 Thr Gly Pro Val Ser Pro His Gln Ile Lys Ser His Thr Leu Thr Thr
237          325          330          335
239 Ser Asp Arg Ala Ala Arg Lys Glu His His Pro Ser His Gly Ala Ser
240          340          345          350
242 Arg Asp Lys Gly His Pro His Gly His Pro Pro Gly Ser Arg Ser Gly
243          355          360          365
245 Tyr Lys Lys Ala Gly Lys Asn Cys Thr Ser His Arg Asn Arg Asn Gln
246          370          375          380
248 Ile Ser Lys Val Ser Ser Gly Lys Glu Leu Thr Glu Leu Gln Asp Tyr
249 385          390          395          400
251 Ala Pro Asp Tyr Gln His Lys Phe Ser Phe Asp Ile Met Pro Thr Ala
252          405          410          415
254 Arg Pro Lys Arg Lys Gly Lys Cys Ala Arg Arg Thr Pro Ile Arg Ala
255          420          425          430
257 Pro Ser Gly Val Gln Gln Ala Ser Ser Gly Thr Ala Leu Gly Ala Pro
258          435          440          445
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261          450          455          460
264 <210> SEQ ID NO: 5
265 <211> LENGTH: 473

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266 <212> TYPE: PRT
267 <213> ORGANISM: Homo sapiens
269 <400> SEQUENCE: 5
270 Met Lys Arg Ala Ser Ala Gly Gly Ser Arg Leu Leu Ala Trp Val Leu
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273 Trp Leu Gln Ala Trp Gln Val Ala Ala Pro Cys Pro Gly Ala Cys Val
274           20           25           30
276 Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln Gly Leu
277           35           40           45
279 Gln Ala Val Pro Val Gly Ile Pro Ala Ala Ser Gln Arg Ile Phe Leu
280           50           55           60
282 His Gly Asn Arg Ile Ser His Val Pro Ala Ala Ser Phe Arg Ala Cys
283   65           70           75           80
285 Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Val Leu Ala Arg Ile
286           85           90           95
288 Asp Ala Ala Ala Phe Thr Gly Leu Ala Leu Leu Glu Gln Leu Asp Leu
289           100          105          110
291 Ser Asp Asn Ala Gln Leu Arg Ser Val Asp Pro Ala Thr Phe His Gly
292           115          120          125
294 Leu Gly Arg Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu
295           130          135          140
297 Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr
298 145           150          155          160
300 Leu Gln Asp Asn Ala Leu Gln Ala Leu Pro Asp Asp Thr Phe Arg Asp
301           165          170          175
303 Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Ser Ser
304           180          185          190
306 Val Pro Glu Arg Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu
307           195          200          205
309 Leu His Gln Asn Arg Val Ala His Val His Pro His Ala Phe Arg Asp
310           210          215          220
312 Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Ala
313 225           230          235          240
315 Leu Pro Thr Glu Ala Leu Ala Pro Leu Arg Ala Leu Gln Tyr Leu Arg
316           245          250          255
318 Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp
319           260          265          270
321 Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Ser
322           275          280          285
324 Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Asn
325           290          295          300
327 Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro Tyr His Pro Ile Trp
328 305           310          315          320
330 Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu Gly Leu Pro Lys Cys Cys
331           325          330          335
333 Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly Arg Pro
334           340          345          350
336 Ala Ser Ala Gly Asn Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Ser
337           355          360          365

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\All6us.app

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L:778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:781 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:790 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:793 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
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L:799 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
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L:808 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:811 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
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L:847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
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